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Figure 1. Sequence of *C. pneumoniae* ATP-binding cassette gene

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acttcccccc tgctaaacta tgctcagata atgctgctat gattgcaggt ctagggggag 60
aaaattttca aaaaaactct agtattccgg aaattcgtat atg cgc aag ata tca 115
                                     Met Arg Lys Ile Ser
                                     1 5

gtg gga atc tgt atc acc att ctc ctt agc ctc tcc gta gtc ctc caa 163
Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu Ser Val Val Leu Gln
                                     10 15 20

ggc tgc aag gag tcc agt cac tcc tct aca tct cgg gga gaa ctc gct 211
Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser Arg Gly Glu Leu Ala
                                     25 30 35

att aat ata aga gat gaa ccc cgt tct tta gat cca aga caa gtg cga 259
Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp Pro Arg Gln Val Arg
                                     40 45 50

ctt ctt tca gaa atc agc ctt gtc aaa cat atc tat gag gga tta gtt 307
Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile Tyr Glu Gly Leu Val
                                     55 60 65

caa gaa aat aat ctt tca gga aat ata gag cct gct ctt gca gaa gac 355
Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro Ala Leu Ala Glu Asp
                                     70 75 80 85

tac tct ctt tcc tcg gac gga ctc act tat act ttt aaa ctg aaa tca 403
Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr Phe Lys Leu Lys Ser
                                     90 95 100

gct ttt tgg agt aat ggc gac ccc tta aca gct gaa gac ttt ata gaa 451
Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala Glu Asp Phe Ile Glu
                                     105 110 115

tct tgg aaa caa gta gct act caa gaa gtc tca gga atc tat gct ttt 499
Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser Gly Ile Tyr Ala Phe
                                     120 125 130

gcc ttg aat cca att aaa aat gta cga aag atc caa gag gga cac ctc 547
Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile Gln Glu Gly His Leu
                                     135 140 145

tcc ata gac cat ttt gga gtg cac tct cct aat gaa tct aca ctt gtt 595
Ser Ile Asp His Phe Gly Val His Ser Pro Asn Glu Ser Thr Leu Val
                                     150 155 160 165

gtt acc ctg gaa tcc cca acc tcg cat ttc tta aaa ctt tta gct ctt 643
Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu Lys Leu Leu Ala Leu
                                     170 175 180

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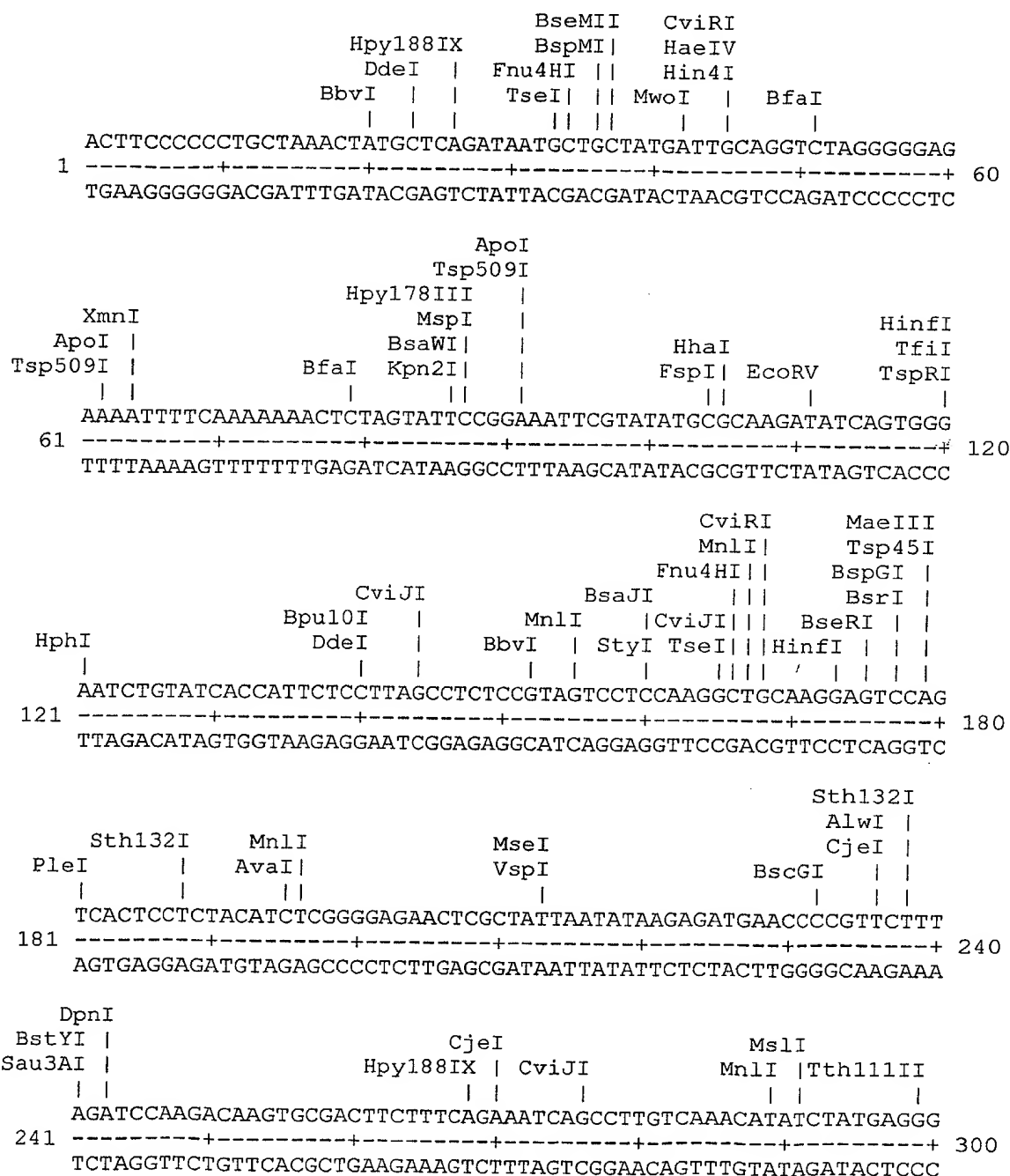
Figure 1 Cont.

cca gtc ttt ttc ccc gtt cat aaa tct caa aga acc ctg caa tcc aaa	691
Pro Val Phe Phe Pro Val His Lys Ser Gln Arg Thr Leu Gln Ser Lys	
185 190 195	
tct cta cct ata gca agc gga gct ttc tat cct aaa aat atc aaa caa	739
Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro Lys Asn Ile Lys Gln	
200 205 210	
aaa caa tgg ata aaa ctc tca aaa aac cct cac tac tat aat caa agt	787
Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His Tyr Tyr Asn Gln Ser	
215 220 225	
cag gtg gaa act aaa acg att acg att cac ttc att ccc gat gca aac	835
Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe Ile Pro Asp Ala Asn	
230 235 240 245	
aca gca gca aaa cta ttt aat cag gga aaa ctc aat tgg caa gga cct	883
Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu Asn Trp Gln Gly Pro	
250 255 260	
cct tgg gga gaa cgc att cct caa gaa acc cta tcc aat tta cag tct	931
Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu Ser Asn Leu Gln Ser	
265 270 275	
aag ggg cac tta cac tct ttt gat gtc gca gga acc tca tgg ctc acc	979
Lys Gly His Leu His Ser Phe Asp Val Ala Gly Thr Ser Trp Leu Thr	
280 285 290	
ttc aat atc aat aaa ttc ccc ctc aac aat atg aag ctt aga gaa gcc	1027
Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met Lys Leu Arg Glu Ala	
295 300 305	
tta gca tca gcc tta gat aag gaa gct ctt gtc tca act ata ttc tta	1075
Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val Ser Thr Ile Phe Leu	
310 315 320 325	
ggc cgt gca aaa act gcc gat cat ctc cta cct aca aat att cat agc	1123
Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro Thr Asn Ile His Ser	
330 335 340	
tat ccc gaa cat caa aaa caa gag atg gca caa cgc caa gct tac gct	1171
Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln Arg Gln Ala Tyr Ala	
345 350 355	
aaa aaa ctc ttt aaa gaa gct tta gaa gaa ctc caa atc act gct aaa	1219
Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu Gln Ile Thr Ala Lys	
360 365 370	
gat ctc gaa cat ctt aat ctt atc ttt ccc gtt tcc tcg tca gca agt	1267
Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val Ser Ser Ser Ala Ser	
375 380 385	

[illegible]

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Figure 2. Restriction enzyme analysis of the *C. pneumoniae* ATP-binding cassette gene



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Figure 2 Cont.

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                                Cac8I
Hpy178III   Hpy178III   CviJI |   CviRI   BbsI
|           |           |   |           |
ATTAGTTCAAGAAAATAATCTTTTCAGGAAATATAGAGCCTGCTCTTGCAGAAGACTACTC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TAATCAAGTTCTTTTATTAGAAAGTCCTTTATATCTCGGACGAGAACGTCTTCTGATGAG

                                Hpy188IX
                                PleI|
BsaJI |   MnlI   DraI   AluI
MboII |   |HinfI|   MseI|   CviJI
|   |   |   |   |   |
TCTTTCCTCGGACGGACTCACTTATACTTTTAAACTGAAATCAGCTTTTTGGAGTAATGG
361 -----+-----+-----+-----+-----+-----+-----+ 420
AGAAAGGAGCCTGCCTGAGTGAATATGAAAATTTGACTTTAGTCGAAAACCTCATTACC

                                AluI
                                CviJI   HinfI   Hpy178III
                                MspAII   MboII Bce83I   SmlI |
SimI   MseI PvuII   BbsI TfiI Eco57I   AluI   |   |
|   |   |   |   |   |   |   |   |   |
CGACCCCTTAACAGCTGAAGACTTTATAGAATCTTGAAACAAGTAGCTACTCAAGAAGT
421 -----+-----+-----+-----+-----+-----+-----+ 480
GCTGGGGAATTGTCGACTTCTGAAATATCTTAGAACCTTTGTTCATCGATGAGTTCTTCA

                                DpnI
                                MnlI|
HinfI   TfiI   MseI   BstYI|
BsmAI |   Tsp509I |   Sau3AI|
Hpy178III|   HinfI |   AlwI   |||
DdeI |||   BseMII   TfiI |   RsaI|   |||
|   |   |   |   |   |   |   |
CTCAGGAATCTATGCTTTTGCCTTGAATCCAATTAAAAATGTACGAAAGATCCAAGAGGG
481 -----+-----+-----+-----+-----+-----+-----+ 540
GAGTCCTTAGATACGAAAACGGAACCTTAGGTTAATTTTTACATGCTTTCTAGGTTCTCCC

                                BseSI
                                BsiHKAI
                                Bsp1286I
                                CviRI |
                                MnlI   MjaIV |   HinfI   BsaJI
                                BsmFI |   ApaLI |   TfiI   EcoRII
                                |   |   |   |   |
ACACCTCTCCATAGACCATTTTGGAGTGCACCTCTCCTAATGAATCTACACTTGTGTGTTAC
541 -----+-----+-----+-----+-----+-----+-----+ 600
TGTGGAGAGGTATCTGGTAAAACCTCACGTGAGAGGATTACTTAGATGTGAACAACAATG

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Figure 2 Cont.

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                                AluI
                                CviJI
                                EarI
HinfI      TfiI      MseI      CjePI |      SapI
ScrFI |      MnlI | MboII |      BsrI |      BscGI
| |      | |      | |      | |      | |
CCTGGAATCCCCAACCTCGCATTTCTTAAACTTTTAGCTCTTCCAGTCTTTTCCCCGT
601 -----+-----+-----+-----+-----+-----+-----+ 660
GGACCTTAGGGGTGGAGCGTAAAGAATTTGAAAATCGAGAAGGTCAGAAAAAGGGCA

                                AluI
                                CviJI
                                MwoI |
                                AciI | |
Sth132I CjePI      CviRI      SfcI      Cac8I | | |
| |      | |      | |      | |      | | |
TCATAAATCTCAAAGAACCCTGCAATCCAAATCTCTACCTATAGCAAGCGGAGCTTTCTA
661 -----+-----+-----+-----+-----+-----+-----+ 720
AGTATTTAGAGTTTCTTGGGACGTTAGGTTTAGAGATGGATATCGTTCGCCTCGAAAGAT

                                Tth111II
                                MnlI
TCCTAAAAATATCAAACAAAAACAATGGATAAACTCTCAAAAAACCCTCACTACTATAA
721 -----+-----+-----+-----+-----+-----+-----+ 780
AGGATTTTTATAGTTTGTTTTGTACCTATTTTGAGAGTTTTTTGGGAGTGATGATATT

                                Sth132I      Fnu4HI
                                HinfI      Hpy178III |      TseI
                                TfiI      SfaNI |      CviRI | MwoI | |
                                | |      | |      | |      | |
TCAAAGTCAGGTGGAACTAAAACGATTACGATTCACTTCATTCCCGATGCAAACACAGC
781 -----+-----+-----+-----+-----+-----+-----+ 840
AGTTTCAGTCCACCTTTGATTTTGCTAATGCTAAGTGAAGTAAGGGCTACGTTTGTGTCG

                                AvaII      MnlI
                                EcoO109I      Bce83I |
                                Psp5II      BslI | |
                                MseI      MunI      Sau96I      BsaJI | |      BsmI
                                BbvI |      Tsp509I      Sse8647I      StyI | |      XmnI
                                | |      | |      | |      | |      | |
AGCAAACTATTTAATCAGGGAAACTCAATTGGCAAGGACCTCCTTGGGGAGAACGCAT
841 -----+-----+-----+-----+-----+-----+-----+ 900
TCGTTTTGATAAATTAGTCCCTTTGAGTTAACCGTTCCCTGGAGGAACCCCTCTTGCGTA

                                BseSI
Hpy178III      Tsp509I      DdeI      Bsp1286I
SmlI |      MnlI |      Bst4CI |      BmgI |
| |      | |      | |      | |
TCCTCAAGAAACCCTATCCAATTTACAGTCTAAGGGCACTTACACTCTTTTGATGTCGC
901 -----+-----+-----+-----+-----+-----+-----+ 960
AGGAGTTCTTTGGGATAGGTTAAATGTCAGATTCCCCGTGAATGTGAGAAAACCTACAGCG

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Figure 2 Cont.

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Figure 2 Cont.

MnlI
CviJI
NlaIII
HphI
NlaIV
ApoI
Tsp509I
DdeI
AluI
CviJI
HindIII
MnlI
961
AGGAACCTCATGGCTCACCTTCAATATCAATAAATCCCCCTCAACAATATGAAGCTTAG
-----+-----+-----+-----+-----+-----+-----+ 1020
TCCTTGGAGTACCGAGTGAAGTTATAGTTATTTAAGGGGGAGTTGTTATACTTCGAATC

Bpu10I SfaNI
DdeI DdeI
CviJI CviJI
AluI BceI
CviJI BsmAI
CviJI DdeI
1021
AGAAGCCTTAGCATCAGCCTTAGATAAGGAAGCTCTTGTCTCAACTATATTCTTAGGCCG
-----+-----+-----+-----+-----+-----+ 1080
TCTTCGGAATCGTAGTCGGAATCTATTCCTTCGAGAACAGAGTTGATATAAGAATCCGGC

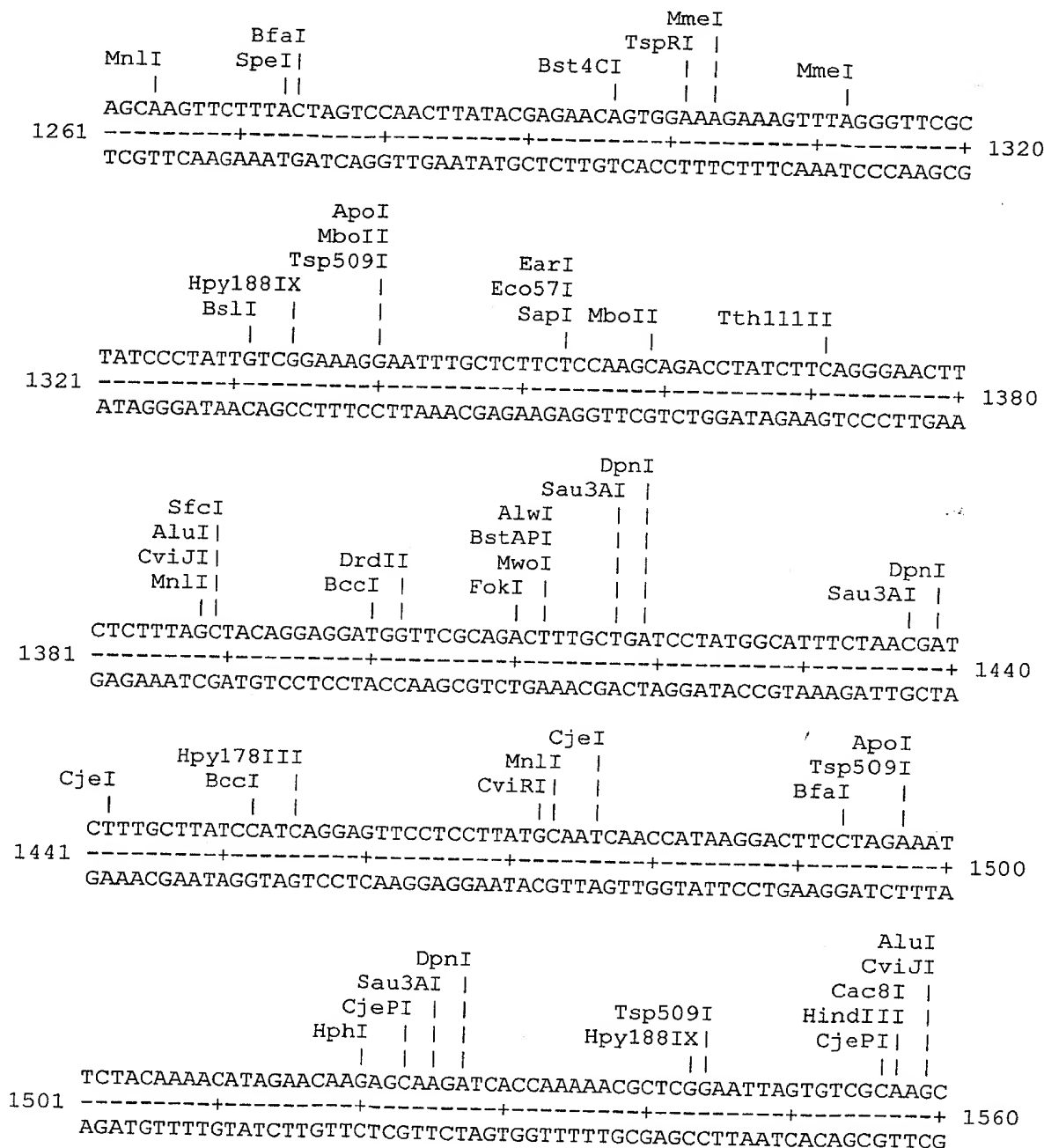
DpnI
Sau3AI
BstAPI
CviRI
Hpy178III
AluI Sth132I
CviJI CjeI
SspI
1081
TGCAAAACTGCCGATCATCTCCTACCTACAAATATTCATAGCTATCCCGAACATCAAAA
-----+-----+-----+-----+-----+-----+ 1140
ACGTTTTTTGACGGCTAGTAGAGGATGGATGTTTATAAGTATCGATAGGGCTTGTAGTTTT

AluI
CviJI
HindIII
DraI
MseI
CjeI
AluI
CviJI
HindIII
DraI
MseI
1141
ACAAGAGATGGCACAACGCCAAGCTTACGCTAAAAAACTCTTTAAAGAAGCTTTAGAAGA
-----+-----+-----+-----+-----+-----+ 1200
TGTTCTCTACCGTGTTGCGGTTCGAATGCGATTTTTTTGAGAAATTTCTTCGAAATCTTCT

TaqI
Hpy178III
DpnI
BglII
BstYI
Sau3AI
TspRI
BtsI
MboII
MseI
Sth132I
BscGI
1201
ACTCCAAATCACTGCTAAAGATCTCGAACATCTTAATCTTATCTTTCCCGTTTCCTCGTC
-----+-----+-----+-----+-----+-----+ 1260
TGAGGTTTAGTGACGATTTCTAGAGCTTGTTAGAATTAGAATAGAAAGGGCAAAGGAGCAG

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Figure 2 Cont.



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Figure 2 Cont.

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          BfaI          DpnI          HgaI
        BsaI |          Sau3AI |          Tsp509I
        BsmAI |          CviJI | |
          | |          | | |
1561 TTCTCTTTACCTAGAGACCTTTTCATATTATTGAGCCGATCTACCACGACGCATTTCAATT
-----+-----+-----+-----+-----+-----+-----+ 1620
AAGAGAAATGGATCTCTGGAAAGTATAATAACTCGGCTAGATGGTGCTGCGTAAAGTTAA

                      HinfI
                      CjeI |
                    HphI | |    PleI
                    BfaI | |    BsmAI |          MjaIV
                      | | |          |
1621 TGCTATGAATAAAAAAAGTTTCTAATCTAGGAGTCTCACCAACAGGAGTTGTGGACTTCCG
-----+-----+-----+-----+-----+-----+ 1680
ACGATACTTATTTTTTGAAGATTAGATCCTCAGAGTGGTTGTCTCAACACCTGAAGGC

Bpu10I
  DdeI          MnlI          HinfI
CjeI | Tsp509I    MseI |          Hpy178III    TfiI TaqII
  | |          | |          |          |          |
1681 TTATGCTAAGGAAAAATTAGCACCTCTTTTAATCTCGCAAAGTTGTCAAGAAGTGAATCTT
-----+-----+-----+-----+-----+-----+ 1740
AATACGATTCCTTTTAATCGTGGAGAAAATTAGAGCGTTTGAACAGTTCTTGACTTAGAA

          NlaIV          NlaIV
        BsrI |          BanI |          Hpy188IX
        BanI | |          BglI | |          MboII |          EarI
        BmrI | | |          MwoI | |          MnlI | |          SapI
          | | |          | | |          | |
1741 ATACTAAAGTGGGTGCCTTTGTGGCACCTCGTTTCCTTCTGACTGCTCTTCTCTCTA
-----+-----+-----+-----+-----+-----+ 1799
TATGATTTGACCCACGGAACACCGTGGAGCAAAGGAAGACTGACGAGAAGAGAGAT

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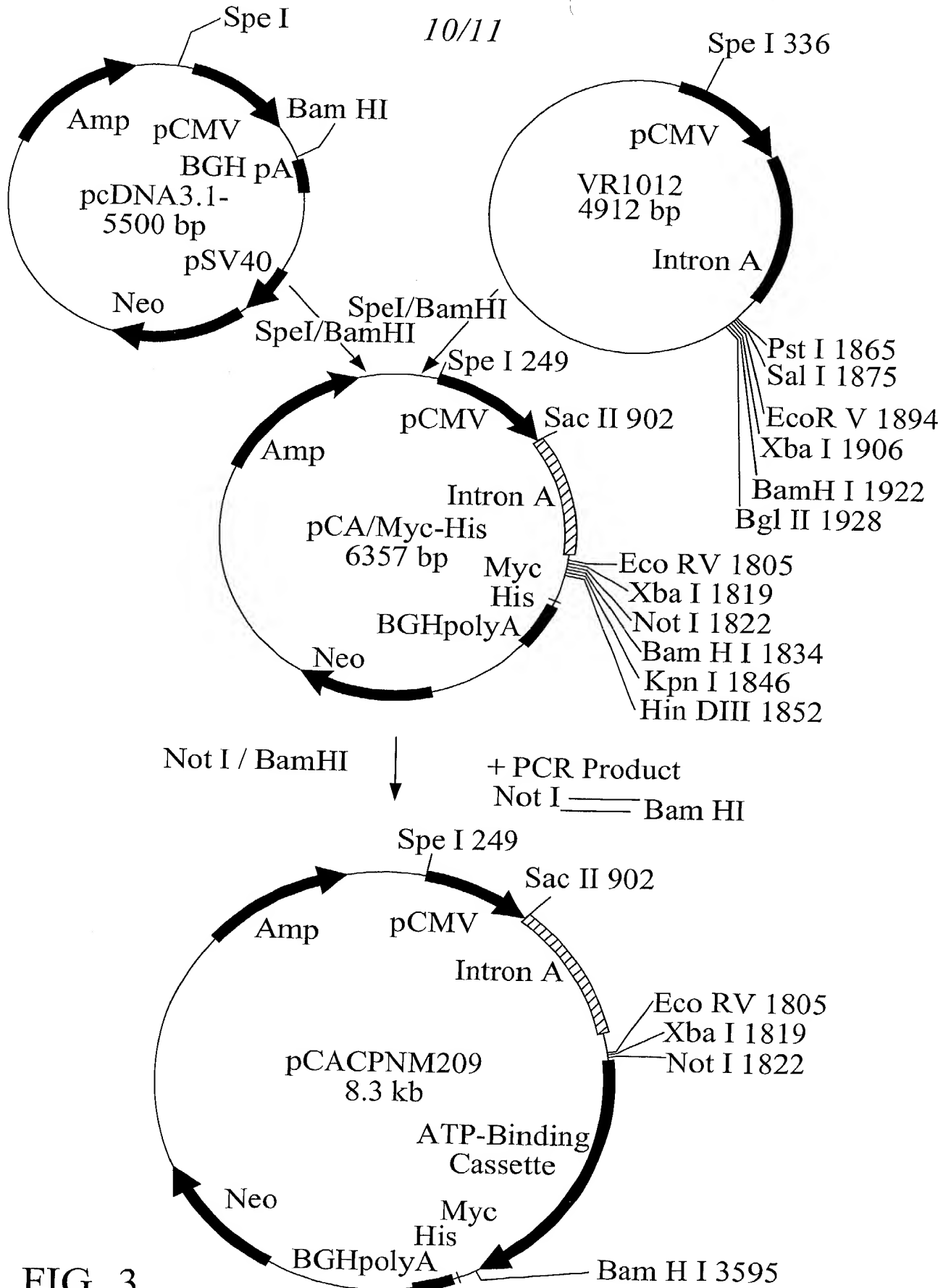


FIG. 3
Construction of pCACPNM209

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Figure 4: Protective efficacy of DNA immunization with pCACP NM209

